

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/Q45784
Source: IFW
Date Processed by STIC: 12/3/4

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/645,784

DATE: 12/03/2004

TIME: 12:08:58

Input Set : N:\CrF3\RULE60\10645784.raw
 Output Set: N:\CRF4\12032004\J645784.raw

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1 <110> APPLICANT: FEIGE, ULRICH
2   LIU, CHUAN-FA
3   CHEETHAM, JANET C.
4   BOONE, THOMAS CHARLES
5   GUDAS, JEAN MARIE
6 <120> TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
7 <130> FILE REFERENCE: A-527A
8 <140> CURRENT APPLICATION NUMBER: US/10/645,784
9 <141> CURRENT FILING DATE: 2003-08-18
10 <150> PRIOR APPLICATION NUMBER: US/09/563,286
11 <151> PRIOR FILING DATE: 2000-05-03
12 <150> PRIOR APPLICATION NUMBER: 09/428,082
13 <151> PRIOR FILING DATE: 1999-10-22
14 <150> PRIOR APPLICATION NUMBER: 60/105,371
15 <151> PRIOR FILING DATE: 1998-10-23
16 <160> NUMBER OF SEQ ID NOS: 1157
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 684
21 <212> TYPE: DNA
22 <213> ORGANISM: HUMAN
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(684)
26 <223> OTHER INFORMATION:
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29   Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
30     1           5           10          15
31   ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      96
32   Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
33     20          25          30
34   atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc      144
35   Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
36     35          40          45
37   cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag      192
38   His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
39     50          55          60
40   gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg      240
41   Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
42     65          70          75          80
43   tac cgt gtg gtc agc gtc acc gtc ctg cac cag gac tgg ctg aat      288
44   Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

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Input Set : N:\Crf3\RULE60\10645784.raw
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45	85	90	95	
46	ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc			336
47	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
48	100	105	110	
49	atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag			384
50	Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
51	115	120	125	
52	gtg tac acc ctg ccc cca tcc cggtt gat gag ctg acc aag aac cag gtc			432
53	Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
54	130	135	140	
55	agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg			480
56	Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
57	145	150	155	160
58	gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct			528
59	Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro			
60	165	170	175	
61	ccc gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc			576
62	Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
63	180	185	190	
64	gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg			624
65	Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
66	195	200	205	
67	atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg			672
68	Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
69	210	215	220	
70	tct ccg ggt aaa			684
71	Ser Pro Gly Lys			
72	225			
74	<210> SEQ ID NO: 2			
75	<211> LENGTH: 228			
76	<212> TYPE: PRT			
77	<213> ORGANISM: HUMAN			
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79	Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu			
80	1	5	10	15
81	Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
82	20	25	30	
83	Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
84	35	40	45	
85	His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu			
86	50	55	60	
87	Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
88	65	70	75	80
89	Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
90	85	90	95	
91	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
92	100	105	110	
93	Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
94	115	120	125	

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95      Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
96          130           135           140
97      Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
98          145           150           155           160
99      Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro
100         165           170           175
101      Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
102          180           185           190
103      Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
104          195           200           205
105      Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
106          210           215           220
107      Ser Pro Gly Lys
108          225
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111 <211> LENGTH: 36
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: PEPTIDE SEQUENCE MODIFIED FOR PEGYLATION
116 <220> FEATURE:
117 <221> NAME/KEY: misc_feature
118 <222> LOCATION: (18)..(18)
119 <223> OTHER INFORMATION: Methoxy-polyethylene glycol (5000 Dalton)-sulfoacetyl group
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120      hed to the sidechain.
121 <400> SEQUENCE: 3
122      Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
123      1           5           10           15
124      Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
125          20           25           30
126      Ala Ala Arg Ala
127          35
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 36
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
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135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (18)..(18)
138 <223> OTHER INFORMATION: Methoxy-polyethylene glycol (5000 Dalton)-succinimidyl group
atta
139      ched to the sidechain.
140 <400> SEQUENCE: 4
141      Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
142      1           5           10           15
143      Gly Cys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
144          20           25           30
145      Ala Ala Arg Ala

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Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

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155 <221> NAME/KEY: CDS
156 <222> LOCATION: (39)...(779)
157 <223> OTHER INFORMATION:
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160                               Met Asp Lys Thr His Thr
161                               1           5
162      tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc      104
163      Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
164      10          15          20
165      ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct      152
166      Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
167      25          30          35
168      gag gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc      200
169      Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val
170      40          45          50
171      aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca      248
172      Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
173      55          60          65          70
174      aag ccg ccg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc      296
175      Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
176      75          80          85
177      ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc      344
178      Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
179      90          95          100
180      aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc      392
181      Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
182      105         110         115
183      aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      440
184      Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
185      120         125         130
186      tcc ccg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc      488
187      Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
188      135         140         145         150
189      aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      536
190      Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
191      155         160         165
192      cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      584
193      Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
194      170         175         180
195      ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg      632

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196	Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp			
197	185	190	195	
198	cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac			680
199	Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His			
200	200	205	210	
201	aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ggt gga			728
202	Asn His Tyr Thr Gln Lys Ser Leu Ser Pro Gly Lys Gly			
203	215	220	225	230
204	ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg gct gct cgt			
205	Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg			776
206	235	240	245	
207	gct taatctcgag gatcc			794
208	Ala			
210	<210> SEQ ID NO: 6			
211	<211> LENGTH: 247			
212	<212> TYPE: PRT			
213	<213> ORGANISM: Artificial Sequence			
214	<220> FEATURE:			
215	<223> OTHER INFORMATION: Fc-TMP			
216	<400> SEQUENCE: 6			
217	Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu			
218	1	5	10	15
219	Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
220	20	25	30	
221	Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
222	35	40	45	
223	His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu			
224	50	55	60	
225	Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
226	65	70	75	80
227	Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
228	85	90	95	
229	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
230	100	105	110	
231	Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
232	115	120	125	
233	Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
234	130	135	140	
235	Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
236	145	150	155	160
237	Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
238	165	170	175	
239	Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
240	180	185	190	
241	Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
242	195	200	205	
243	Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
244	210	215	220	
245	Ser Pro Gly Lys Gly Gly Ile Glu Gly Pro Thr Leu Arg			

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/645,784

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TIME: 12:08:59

Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 6,7,8
Seq#:45; Xaa Pos. 8,9,10
Seq#:56; Xaa Pos. 8,9
Seq#:57; Xaa Pos. 8,9,10
Seq#:58; Xaa Pos. 8,9,10,11
Seq#:59; Xaa Pos. 8,9,10,11,12
Seq#:60; Xaa Pos. 8,9,10,11,12,13
Seq#:71; Xaa Pos. 2,12
Seq#:72; Xaa Pos. 2,3,13
Seq#:73; Xaa Pos. 2,12,13
Seq#:74; Xaa Pos. 2,3,13,14
Seq#:83; Xaa Pos. 2,4,5,8,11,13
Seq#:84; Xaa Pos. 2,4,5,8,11,13,16,18,19,22,25,27
Seq#:85; Xaa Pos. 2,4,5,8,11,13
Seq#:86; Xaa Pos. 2,4,5,8,11,13
Seq#:100; Xaa Pos. 4
Seq#:101; Xaa Pos. 1,5
Seq#:102; Xaa Pos. 1,4
Seq#:104; Xaa Pos. 4
Seq#:124; Xaa Pos. 1,2,3,6,9,10
Seq#:142; Xaa Pos. 2,4,8,9
Seq#:212; Xaa Pos. 1,2,3,5,7,8,9
Seq#:221; Xaa Pos. 10
Seq#:222; Xaa Pos. 10
Seq#:223; Xaa Pos. 11
Seq#:224; Xaa Pos. 10
Seq#:225; Xaa Pos. 10
Seq#:226; Xaa Pos. 10
Seq#:227; Xaa Pos. 10
Seq#:228; Xaa Pos. 10
Seq#:229; Xaa Pos. 6,10
Seq#:230; Xaa Pos. 6,10
Seq#:234; Xaa Pos. 5,10
Seq#:235; Xaa Pos. 5,10
Seq#:236; Xaa Pos. 6,10
Seq#:237; Xaa Pos. 5,10
Seq#:240; Xaa Pos. 10
Seq#:241; Xaa Pos. 10
Seq#:242; Xaa Pos. 8,10
Seq#:243; Xaa Pos. 10
Seq#:244; Xaa Pos. 10
Seq#:245; Xaa Pos. 10
Seq#:246; Xaa Pos. 10
Seq#:247; Xaa Pos. 10

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

Seq#:248; Xaa Pos. 10
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Seq#:253; Xaa Pos. 10
Seq#:254; Xaa Pos. 5,10
Seq#:255; Xaa Pos. 6,10
Seq#:256; Xaa Pos. 5,10
Seq#:258; Xaa Pos. 1,10

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 119
Seq#:4; Line(s) 138
Seq#:26; Line(s) 1083,1087
Seq#:27; Line(s) 1101
Seq#:28; Line(s) 1115,1120
Seq#:29; Line(s) 1137
Seq#:30; Line(s) 1155
Seq#:31; Line(s) 1170
Seq#:32; Line(s) 1189,1193
Seq#:85; Line(s) 1789
Seq#:93; Line(s) 1895
Seq#:96; Line(s) 1937
Seq#:97; Line(s) 1953
Seq#:98; Line(s) 1971
Seq#:99; Line(s) 1986
Seq#:100; Line(s) 2001
Seq#:103; Line(s) 2048
Seq#:104; Line(s) 2062
Seq#:124; Line(s) 2270,2282,2291
Seq#:275; Line(s) 4171
Seq#:320; Line(s) 4721
Seq#:377; Line(s) 5471
Seq#:378; Line(s) 5480
Seq#:379; Line(s) 5489
Seq#:380; Line(s) 5498
Seq#:381; Line(s) 5507
Seq#:382; Line(s) 5516
Seq#:383; Line(s) 5525
Seq#:386; Line(s) 5574
Seq#:387; Line(s) 5585
Seq#:388; Line(s) 5594
Seq#:389; Line(s) 5617
Seq#:398; Line(s) 5737
Seq#:419; Line(s) 5973
Seq#:421; Line(s) 6026
Seq#:448; Line(s) 6349
Seq#:461; Line(s) 6516

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/03/2004
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Input Set : N:\Crfr3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

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Seq#:593; Line(s) 8048
Seq#:594; Line(s) 8065,8070,8074
Seq#:909; Line(s) 11479,11483
Seq#:910; Line(s) 11517,11521
Seq#:917; Line(s) 11671
Seq#:1042; Line(s) 13457,13467,13487
Seq#:1110; Line(s) 14871
Seq#:1142; Line(s) 15203,15207,15212,15216
Seq#:1143; Line(s) 15232,15236,15241,15245
Seq#:1144; Line(s) 15261,15265,15270,15274
Seq#:1145; Line(s) 15290,15294,15299,15303
Seq#:1146; Line(s) 15319,15323,15328,15332

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/645,784

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 Output Set: N:\CRF4\12032004\J645784.raw

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 L:158 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
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 L:368 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:0
 L:476 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:0
 L:602 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:0
 L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:0
 L:808 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:0
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 L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
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 L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
 M:341 Repeated in SeqNo=84
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 L:1809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
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 L:2068 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0
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 L:2480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
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 L:3360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:221 after pos.:0
 L:3375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:222 after pos.:0
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 L:3403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:224 after pos.:0
 L:3417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:225 after pos.:0
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 L:3565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:236 after pos.:0
 L:3580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:237 after pos.:0
 L:3624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:0
 L:3646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:241 after pos.:0

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/645,784

DATE: 12/03/2004

TIME: 12:08:59

Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

L:3668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:0
L:3686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:243 after pos.:0
L:3704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:244 after pos.:0
L:3722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:0
L:3740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:246 after pos.:0
L:3762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:247 after pos.:0
L:3784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:248 after pos.:0
L:3806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249 after pos.:0
L:3867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:253 after pos.:0
L:3891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:254 after pos.:0
L:3909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:255 after pos.:0
L:5347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:367,Line#:0
L:5441 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:375,Line#:0
L:5539 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:384,Line#:0
L:5688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:394,Line#:0
L:5781 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:402,Line#:0
L:5924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:416,Line#:0
L:13663 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1055,Line#:0
L:13763 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1057,Line#:0
L:13863 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1059,Line#:0
L:13963 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1061,Line#:0
L:14063 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1063,Line#:0
L:14164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1065,Line#:0
L:14265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1067,Line#:0
L:14364 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1069,Line#:0
L:14983 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1120,Line#:0